IFWO

RAW SEQUENCE LISTING   DATE: 08/27/2004
PATENT APPLICATION: **US/10/730,034**   TIME: 14:25:50

Input Set : **N:\Crf3\RULE60\10730034.raw**
Output Set: **N:\CRF4\08272004\J730034.raw**

SEQUENCE LISTING
```
 3  (1)  GENERAL INFORMATION:
 5       (i)  APPLICANT: Takanori OKURA
 6                       Kakuji TORIGOE
 7                       Masahi KURIMOTO
 9      (ii)  TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
10                               OF INDUCING THE PRODUCTION OF INTERFERON-
12     (iii)  NUMBER OF SEQUENCES: 35
14      (iv)  CORRESPONDENCE ADDRESS:
15            (A)  ADDRESSEE: BROWDY AND NEIMARK
16            (B)  STREET: 419 Seventh Street, N.W., Suite 300
17            (C)  CITY: Washington
18            (D)  STATE: D.C.
19            (E)  COUNTRY: USA
20            (F)  ZIP: 20004
22       (v)  COMPUTER READABLE FORM:
23            (A)  MEDIUM TYPE: Floppy disk
24            (B)  COMPUTER: IBM PC compatible
25            (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
26            (D)  SOFTWARE: Patent In Release #1.0, Version #1.30
28      (vi)  CURRENT APPLICATION DATA:
29            (A)  APPLICATION NUMBER: US/10/730,034
30            (B)  FILING DATE: 09-Dec-2003
31            (C)  CLASSIFICATION: 435
33     (vii)  PRIOR APPLICATION DATA:
34            (A)  APPLICATION NUMBER: US/08/884,324
35            (B)  FILING DATE: 27-JUN-1997
36            (A)  APPLICATION NUMBER: JP 185,305/96
37            (B)  FILING DATE: 27-JUN-1996
39    (viii)  ATTORNEY/AGENT INFORMATION:
40            (A)  NAME: BROWDY, Roger L.
41            (B)  REGISTRATION NUMBER: 25,618
42            (C)  REFERENCE/DOCKET NUMBER: OKURA=1
44      (ix)  TELECOMMUNICATION INFORMATION:
45            (A)  TELEPHONE: 202-628-5197
46            (B)  TELEFAX: 202-737-3528
48  (2)  INFORMATION FOR SEQ ID NO: 1:
50       (i)  SEQUENCE CHARACTERISTICS:
51            (A)  LENGTH: 157 amino acids
52            (B)  TYPE: amino acid
53            (D)  TOPOLOGY: linear
55      (ii)  MOLECULE TYPE: peptide
57      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
```

C--> 29
C--> 30
W--> 34
W--> 36

ENTERED

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PATENT APPLICATION:  US/10/730,034    TIME: 14:25:50

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```

```
      59 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
      60 1             5                 10                  15
      61 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
      62         20              25                  30
      63 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
      64         35              40                  45
      65 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
      66     50              55                  60
W--> 67 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile
      68 65              70                  75                  80
      69 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
      70             85                  90                  95
      71 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
      72             100             105             110
      73 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
      74         115             120             125
      75 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
      76     130             135             140
      77 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
      78 145             150             155
      80 (2) INFORMATION FOR SEQ ID NO: 2:
      82     (i) SEQUENCE CHARACTERISTICS:
      83         (A) LENGTH: 1120 base pairs
      84         (B) TYPE: nucleic acid
      85         (C) STRANDEDNESS: double
      86         (D) TOPOLOGY: linear
      88     (ii) MOLECULE TYPE: cDNA to mRNA
      90    (iii) HYPOTHETICAL: No
      92     (iv) ANTI-SENSE: No
      94     (vi) ORIGINAL SOURCE:
      95         (A) ORGANISM: human
      96         (F) TISSUE TYPE: liver
C--> 98     (ix) FEATURE:
     102         (A) NAME/KEY: leader peptide
     100         (B) LOCATION: 1..177
     101         (C) IDENTIFICATION METHOD: E
     112     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
     114 GCCTGGACAG TCAGCAAGGA ATTGTCTCCC AGTGCATTTT GCCCTCCTGG CTGCCAACTC      60
     115 TGGCTGCTAA AGCGGCTGCC ACCTGCTGCA GTCTACACAG CTTCGGGAAG AGGAAAGGAA     120
     116 CCTCAGACCT TCCAGATCGC TTCCTCTCGC AACAAACTAT TTGTCGCAGG AATAAAG        177
     117 ATG GCT GCT GAA CCA GTA GAA GAC AAT TGC ATC AAC TTT GTG GCA ATG      225
     118 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
     119     -35              -30                 -25
     120 AAA TTT ATT GAC AAT ACG CTT TAC TTT ATA GCT GAA GAT GAT GAA AAC      273
     121 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
     122 -20              -15                 -10                 -5
     123 CTG GAA TCA GAT TAC TTT GGC AAG CTT GAA TCT AAA TTA TCA GTC ATA      321
     124 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
     125             1               5                   10
```

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Input Set : **N:\Crf3\RULE60\10730034.raw**
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```
         126 AGA AAT TTG AAT GAC CAA GTT CTC TTC ATT GAC CAA GGA AAT CGG CCT    369
         127 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
         128         15                  20                  25
         129 CTA TTT GAA GAT ATG ACT GAT TCT GAC TGT AGA GAT AAT GCA CCC CGG    417
         130 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
         131     30                  35                  40
         132 ACC ATA TTT ATT ATA AGT ATG TAT AAA GAT AGC CAG CCT AGA GGT ATG    465
         133 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
         134 45                  50                  55                  60
         135 GCT GTA ACT ATC TCT GTG AAG TGT GAG AAA ATT TCA AYT CTC TCC TGT    513
W--> 136 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
         137             65                  70                  75
         138 GAG AAC AAA ATT ATT TCC TTT AAG GAA ATG AAT CCT CCT GAT AAC ATC    561
         139 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
         140             80                  85                  90
         141 AAG GAT ACA AAA AGT GAC ATC ATA TTC TTT CAG AGA AGT GTC CCA GGA    609
         142 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
         143         95                  100                 105
         146 CAT GAT AAT AAG ATG CAA TTT GAA TCT TCA TCA TAC GAA GGA TAC TTT    657
         147 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
         148     110                 115                 120
         149 CTA GCT TGT GAA AAA GAG AGA GAC CTT TTT AAA CTC ATT TTG AAA AAA    705
         150 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
         151 125                 130                 135                 140
         152 GAG GAT GAA TTG GGG GAT AGA TCT ATA ATG TTC ACT GTT CAA AAC GAA    753
         153 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
         154                 145                 150                 155
         155 GAC TAGCTATTAA AATTTCATGC CGGGCGCAGT GGCTCACGCC TGTAATCCCA     806
         156 Asp
         157 GCCCTTTGGG AGGCTGAGGC GGGCAGATCA CCAGAGGTCA GGTGTTCAAG ACCAGCCTGA  866
         158 CCAACATGGT GAAACCTCAT CTCTACTAAA AATACTAAAA ATTAGCTGAG TGTAGTGACG  926
         159 CATGCCCTCA ATCCCAGCTA CTCAAGAGGC TGAGGCAGGA GAATCACTTG CACTCCGGAG  986
         160 GTAGAGGTTG TGGTGAGCCG AGATTGCACC ATTGCGCTCT AGCCTGGGCA ACAACAGCAA 1046
         161 AACTCCATCT CAAAAAATAA AATAAATAAA TAAACAAATA AAAAATTCAT AATGTGAAAA 1106
         162 AAAAAAAAAA AAAA                                                  1120
         164 (2) INFORMATION FOR SEQ ID NO: 3:
         166      (i) SEQUENCE CHARACTERISTICS:
         167          (A) LENGTH: 135 base pairs
         168          (B) TYPE: nucleic acid
         169          (C) STRANDEDNESS: double
         170          (D) TOPOLOGY: linear
         172     (ii) MOLECULE TYPE: Genomic DNA
         174     (vi) ORIGINAL SOURCE:
         175          (A) ORGANISM: human
         176          (F) TISSUE TYPE: placenta
C--> 178     (ix) FEATURE:
         179          (A) NAME/KEY: exon
         180          (B) LOCATION: 1..135
         181          (C) IDENTIFICATION METHOD: S
```

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                    RAW SEQUENCE LISTING              DATE: 08/27/2004
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                    Input Set : N:\Crf3\RULE60\10730034.raw
                    Output Set: N:\CRF4\08272004\J730034.raw


183      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
185   AA AAC CTG GAA TCA GAT TAC TTT GGC AAG CTT GAA TCT AAA TTA TCA        47
186 Glu Asn Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser
187    -5                     1            5                   10
188 GTC ATA AGA AAT TTG AAT GAC CAA GTT CTC TTC ATT GAC CAA GGA AAT        95
189 Val Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn
190               15              20                  25
191 CGG CCT CTA TTT GAA GAT ATG ACT GAT TCT GAC TGT AGA G                  135
192 Arg Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp
193          30              35                  40
195 (2) INFORMATION FOR SEQ ID NO: 4:
197      (i) SEQUENCE CHARACTERISTICS:
198          (A) LENGTH: 134 base pairs
199          (B) TYPE: nucleic acid
200          (C) STRANDEDNESS: double
201          (D) TOPOLOGY: linear
203     (ii) MOLECULE TYPE: Genomic DNA
205     (vi) ORIGINAL SOURCE:
206          (A) ORGANISM: human
207          (F) TISSUE TYPE: placenta
C--> 209     (ix) FEATURE:
210          (A) NAME/KEY: exon
211          (B) LOCATION: 1..134
212          (C) IDENTIFICATION METHOD: S
215     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
217   AT AAT GCA CCC CGG ACC ATA TTT ATT ATA AGT ATG TAT AAA GAT AGC       47
218 Asp Asn Ala Pro Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser
W--> 219 40                  45              50                  55
220 CAG CCT AGA GGT ATG GCT GTA ACT ATC TCT GTG AAG TGT GAG AAA ATT       95
221 Gln Pro Arg Gly Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile
W--> 222              60              65                  70
223 TCA ACT CTC TCC TGT GAG AAC AAA ATT ATT TCC TTT AAG                   134
224 Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys
W--> 225          80              85
227 (2) INFORMATION FOR SEQ ID NO: 5:
229      (i) SEQUENCE CHARACTERISTICS:
230          (A) LENGTH: 87 base pairs
231          (B) TYPE: nucleic acid
232          (C) STRANDEDNESS: double
233          (D) TOPOLOGY: linear
235     (ii) MOLECULE TYPE: Genomic DNA
237     (vi) ORIGINAL SOURCE:
238          (A) ORGANISM: human
239          (F) TISSUE TYPE: placenta
C--> 241     (ix) FEATURE:
242          (A) NAME/KEY: exon
243          (B) LOCATION: 1..87
244          (C) IDENTIFICATION METHOD: S
246     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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```
248 GAATAAAG ATG GCT GCT GAA CCA GTA GAA GAC AAT TGC ATC AAC TTT GTG    50
249          Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val
250              -35              -30              -25
251 GCA ATG AAA TTT ATT GAC AAT ACG CTT TAC TTT ATA G                    87
252 Ala Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala
253      -20              -15              -10
255 (2) INFORMATION FOR SEQ ID NO: 6:
257      (i) SEQUENCE CHARACTERISTICS:
258          (A) LENGTH: 12 base pairs
259          (B) TYPE: nucleic acid
260          (C) STRANDEDNESS: double
261          (D) TOPOLOGY: linear
263      (ii) MOLECULE TYPE: Genomic DNA
265      (vi) ORIGINAL SOURCE:
266          (A) ORGANISM: human
267          (F) TISSUE TYPE: placenta
```
C--> 269   **(ix) FEATURE:**
```
270          (A) NAME/KEY: exon
271          (B) LOCATION: 1..87
272          (C) IDENTIFICATION METHOD: S
274      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
276   CT GAA GAT GAT G                                                    12
277 Ala Glu Asp Asp Glu
278 -10
280 (2) INFORMATION FOR SEQ ID NO: 7:
282      (i) SEQUENCE CHARACTERISTICS:
283          (A) LENGTH: 2167 base pairs
284          (B) TYPE: nucleic acid
285          (C) STRANDEDNESS: double
286          (D) TOPOLOGY: linear
288      (ii) MOLECULE TYPE: Genomic DNA
290      (vi) ORIGINAL SOURCE:
291          (A) ORGANISM: human
292          (F) TISSUE TYPE: placenta
```
C--> 294   **(ix) FEATURE:**
```
295          (A) NAME/KEY: exon + 3'UTR
296          (B) LOCATION: 1..2167
297          (C) IDENTIFICATION METHOD: E
299      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
301 GAA ATG AAT CCT CCT GAT AAC ATC AAG GAT ACA AAA AGT GAC ATC ATA    48
302 Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys Ser Asp Ile Ile
```
W--> 303 85   90   95   100
```
304 TTC TTT CAG AGA AGT GTC CCA GGA CAT GAT AAT AAG ATG CAA TTT GAA    96
305 Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys Met Gln Phe Glu
```
W--> 306   105   110   115
```
307 TCT TCA TCA TAC GAA GGA TAC TTT CTA GCT TGT GAA AAA GAG AGA GAC   144
308 Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu Lys Glu Arg Asp
```
W--> 309   120   125   130
```
310 CTT TTT AAA CTC ATT TTG AAA AAA GAG GAT GAA TTG GGG GAT AGA TCT   192
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/27/2004
PATENT APPLICATION: **US/10/730,034**   TIME: 14:25:51

Input Set : **N:\Crf3\RULE60\10730034.raw**
Output Set: **N:\CRF4\08272004\J730034.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.73
Seq#:2; Xaa Pos.73

VERIFICATION SUMMARY   DATE: 08/27/2004
PATENT APPLICATION: **US/10/730,034**   TIME: 14:25:51

Input Set : **N:\Crf3\RULE60\10730034.raw**
Output Set: **N:\CRF4\08272004\J730034.raw**

```
L:29  M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30  M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36  M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:67  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:64
L:98  M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:102 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:105 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:108 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:513
L:178 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:209 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:241 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:269 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:294 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:364 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:409 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:511 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:681 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:726 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:805 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:809 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:812 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:815 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:818 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:821 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:824 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:827 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:830 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:833 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:836 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:839 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:874 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 13
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:933 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 13
L:934 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:940 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:943 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:966 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 13
L:967 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
```

VERIFICATION SUMMARY   DATE: 08/27/2004
PATENT APPLICATION: **US/10/730,034**   TIME: 14:25:51

Input Set : **N:\Crf3\RULE60\10730034.raw**
Output Set: **N:\CRF4\08272004\J730034.raw**

```
L:970 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:976 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1056 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1059 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1062 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1071 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:1087 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1091 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1094 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1097 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1100 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1103 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1106 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1109 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1112 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1115 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1118 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1121 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME/KEY:] of (2)(ix)
L:1417 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 14
L:1418 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1476 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 14
L:1477 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1509 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 14
L:1510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1516 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1599 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1602 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1605 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1608 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1611 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:1614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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